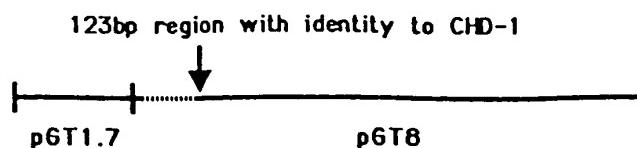


**Figure 1.**

CCCGGTCCGAGGTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGCTAGTTGAC 60  
AAGGTGATGGTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTCCAGCCTTAAT 120  
AATTCTATGAATTCTGTAATTTATTCTTGATCTTTGAGCGAAGTTGTTGGGGATT 180  
TTAGTTGGTTCCCTGTCACTGTTCTTCCTGAAACTGACTTCATTCACATG 240  
AGAATTGCTGTATTGTCAGGTTACAAGTAGTGCAATGGCTGCTAGAAGTAGTGAGAAA 300  
CATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTGCCAAACTGTAGCTTGGG 360  
ATTTGAGGAGCCACAGAGTTGTATATAAATTGTTAATGATATCCTGCCCTGCCTTCC 420  
ATTAATTGCTTGTATGAAACCCTTTTTTTTTTTGGCTTCA 480  
TATCCTGTGTAATGAGTTAATGCATTTAGAACATGGCAGAACTAGGAGATCTGTGG 540  
ATGACAGTGGTACAGGAGCTGAAATTAGATAAAACTATGAGAGTGAAACAGAAAAT 600  
CTGAGGCTAGTTCTTGAGCTGACTGTAATTGTGAGAATATTTCAAGACTACATTA 660  
GTTGTGTGTTGAGGAAAAATAAAATGTTAAGTTGTCCTGAAACCTCCGACC 720  
GGG 723

**Figure 2.**



**Figure 3.**

M	<i>CBD-1</i>	ATTCTTCCAG	ATGATCCTGA	TAAGGAAACCA	CAAGGAAAAC	AGTTACAGAC
C	<i>CBD-1A</i>	ATTTTACCTG	ATGATCCAGA	CAAGGAAACCC	CAGGGCAAAGC	AGCTACAGAC
C	<i>CBD-W</i>	ATTTTACCTG	ATGATCCAGA	TAAGGAAACCC	CAGGGCTAACG	AGTTACAGAC
GT	<i>CBD-W</i>	ATTTTACCTG	ATGACCCAGA	TAAGGAAACCA	CAGGGCAAAGC	AGTTGCAGAC

M	<i>CBD-1</i>	CAAAAAACCA	CAAGCAAAC	AGTTACAGAC	CCGTGCAGAC	TACCTCATCA
C	<i>CBD-1A</i>	CAAGAAACCC	CAGGCAAAGC	AGCTACAGAC	CCGTGCAGAC	TACCTCATTA
C	<i>CBD-W</i>	CAAGAAACCC	CAGGCTAAGC	AGTTACAGAC	CCGTGCAGAT	TACCTCATTA
GT	<i>CBD-W</i>	CAAGAAACCA	CAGGCAAAGC	AGTTGCAGAC	CCGTGCAGAT	TACCTCATTA

M	<i>CHD-1</i>	AACTACTTAG	CAGAGATCTT	GCAAAAAGAG	AGGCTCAGAG	ACTTTGCTGGT	GCG
C	<i>CHD-1A</i>	AATTACTGAA	TAAGACCTT	GCAAGAAAAG	AAGCACAAAG	GCTTGCTGGT	GCA
C	<i>CHD-W</i>	AATTACTGAA	TAAGACCTT	GCAAGAAAAG	AAGCACAGAG	ACTTGCTGGT	GCA
GT	<i>CHD-W</i>	AATTACTGAA	TAAGACCTT	GCAAGAAAAG	AAGTGCAAAG	ACTTACTGGT	GCA

M	<i>CHD-1</i>	ILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREAQRLCGA
C	<i>CHD-1A</i>	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA
C	<i>CHD-W</i>	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA
GT	<i>CHD-W</i>	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEVQRLTGA *****

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**Figure 4.**

Figure 5.

1 CGGGCTGCCG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG  
 51 AAGGCCTGGC CCGCCGAGCC GGACGCACGC AGGTATTG GCAAAATCT  
 101 TGGCCATCTG TAGAGAATAG CAAGTCAAAC GCATTACTTC GAAAACATAC  
 151 GGAGTACCAAG AAAGGGGATT CTTGACCTAC ACCTTGTAAC CTGAGTGGAC  
 201 TTCTTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA GTGATGAAGA  
 251 AAGTGTAAAG AACAGCAGTG GAGAGTCAG CAGATCAGAT GATGATTCTG  
 301 GGTCACTTC AGGTCTGGA TCTGGTCAA GCTCTGAAAG CAGTAGCGAT  
 351 GGAAGTAGCA GCCAGTCAGG TAGCAGTGC TCTGAATCTG GTTCAGAGTC  
 401 AGGCAGTCAA TCCGAATCAG AGTCTGACAC ATCTAGAGAG AAGAAACAAG  
 451 TTCAAGCTAA ACCTCCGAAA GCTGACGGAT CTGAGTTTG GAAGTCCAGT  
 501 CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA AGCAACAGCA  
 551 ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAACAG GACTCATCCA  
 601 GTAGTGAAGA TTCTGCCGAT GATTGTCGA GTGAAACTAA GAAGAAAAAG  
 651 CATAAAAGATG AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC  
 701 TGTTCTGTAT TCTGAATCGG CGGAAGATGG GGATAAAAAG AGTTGTGAAG  
 751 AAAGTGAATC TGACTATGAG CCAAAAAACA AAGTCAAAG CCGTAAACCT  
 801 CCAAGCAGAA TTAAGCCAAA AAGTGGAAA AAGAGCACAG GACAGAAGAA  
 851 GAGGCAACTT GATTTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG  
 901 ATAAGAGAGG ATCTCGTCG CAGGCAACAG TGAATGTTAG TTACAAAGAA  
 951 GCTGAAGAAA CCAAGACAGA TTCTGATGAT TTGCTGGAG TTTGTGGAGA  
 1001 GGATGTCCCA CAGACTGAAG AAGATGAATT TGAAACTATA GAGAAGTTA  
 1051 TGACAGTCG ATTGGCCGA AAAGGAGCCA CTGGTGCCTC AACCACCATC  
 1101 TATGCCGTT AGGCAGATGG TGACCCAAAT GCTGGGTTTG AAAAGTCAAA  
 1151 GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGAAAGGC TGGTCACACA  
 1201 TCCATAAACAC TTGGGAACT GAAGAACGC TGAAGCAACA AAATGTTAAA  
 1251 GGAATGAACA AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG  
 1301 CTGGCTGAAA AATGCTCTC CAGAAGATGT GGAATATTAT AACTGCCAGC  
 1351 AGGAGCTTAC AGATGATCTG CACAAACAAT ATCAAATAGT GGAAAGAATA  
 1401 ATTGCTCATT CAAATCAAA GTCAGCAGCT GGTTATCCGG ACTACTATTG  
 1451 CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGAA GATGGTGCTC  
 1501 TCATTGCCAA AAAGTTTCAG GCACGCATTG ATGAGTATT TAGCAGAAAT  
 1551 CAATCCAAGA CTACTCCCT TAAGGACTGC AAGGTTCTAA AACAGAGACC  
 1601 AAGATTTGTT GCACTGAAGA AGCAACATC TTACATTGGA GGACATGAAA  
 1651 GTCTGGAGTT AAGAGATTAT CAGTTAAATG GATTGAATTG GCTCGCTCAT  
 1701 TCATGGTGCA AAGGAAATAG TTGTATTCTT GCAGATGAAA TGGGCTGGG  
 1751 TAAACAAATA CAAACAAATT CTTTCTGAA CTACCTGTT CATGACACATC  
 1801 AACTGTATGG CCCTTTCTT CTGCGCGTGC CACTTTCTAC CTTGACATCT  
 1851 TGGCAAAGAG AGATTCAAAC TTGGCTCCT CAGATGAATG CTGTAGTTA  
 1901 CTTAGGAGAT ATAACTAGTA GAAATATGAT AAGGACTCAT GAATGGATGC  
 1951 ATCCACAGAC TAAACGATTA AAGTTAACAA TACTTCTGAC GACATATGAA  
 2001 ATTTTACTGA AGGATAAGTC ATTCCCTGGT GGTCTCAATT GGGCATTCT  
 2051 AGGAGTTGAT GAAGCTCATC GTTTAAAAAA TGATGACTCT CTTCTGTACA  
 2101 GGACTTAAT AGACTTTAAG TCCAACCATC GACTTCTGAT TACTGGAAAC  
 2151 CCACTGCAA ATTCCCTCAA AGAGCTGTGG TCTTGTGTC ATTTCATCAT  
 2201 GCCAGAAAAA TTTTCCCTCT GGGAGATTG TGAAGAGGAG CATGCCAAAG  
 2251 GAAGAGAGTA TGTTTATGCA AGTCTTCACA AAGAGCTGAA ACCATTTTA  
 2301 CTAAGAAGAG TTAAAAAAAAG TGAGAAAAG TCTTACCTG CTAAGGTTGA  
 2351 ACAATTCTG AGGATGGAAA TGAGTGCATT GCAGAAGCAA TATTACAAGT  
 2401 GGATTTAAC AAGGAATTAT AAAGCCCTCA GTAAAGGTT AAAAGGCAGT  
 2451 ACCTCAGGCT TTCTGAAACAT TATGATGGAA CTTAAGAAGCT GTTGTAAACCA  
 2501 TTGCTACCTC ATTAAGCCAC CAGATGATAA TGAATTCTAT AATAAACAGG  
 2551 AGGCCTTACA GCATTGATA CGTAGCAGCG GGAAACTAAT CCTTCTTGAC  
 2601 AAGCTACTGA TTCGTCTGCCG AGAACGTGGC AACAGAGTTC TGATTTCTC  
 2651 TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATGCC  
 2701 AGTTCCCTT CCAGAGACTT GATGGATCAA TAAAAGGGGA ATTGAGGAAG  
 2751 CAAGCACTGG ATCATTCTAA TGCAGAAGGA TCAGAGGATT TCTGTTTTT  
 2801 ACTGCTACA AGAGCTGGAG GATTAGGTAT TAACTTGGCA TCTGCTGACA  
 2851 CTGAGTTAT TTTGATTCT GACTCGAAC CACAGAATGA TCTGCAGGCA  
 2901 CAGGCAGAG CTCATAGAAT TGGACAGAAG AACACAGGTTA ATATTATCG  
 2951 GCTAGTCACA AAAGGATCAG TAGAAGAAGA TATTCTGAA AGAGCCAAGA

3001 AGAAGATGGT GCTAGACCATTAGTAATTC AGAGAAATGGA CACGACAGGA  
 3051 AAAACTGTTCTGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTAA  
 3101 TAAAGAAGAG TTATCAGCTA TTTTGAAGTT TGCGTGTGAG GAACTCTTA  
 3151 AAGAACCTGA AGGAGAAGAA CAGGAGCCCC AGGAAATGGA TATAGATGAA  
 3201 ATCTTGAAAGA GAGCTGAAAC TCAGGGAAAAT GAGCCAGGTC CATTGACTGT  
 3251 AGGGGATGAG TTGCTTTCAC AGTTCAAGGT GGCGAACTTT TCCAATATGG  
 3301 ATGAAGATGAA TATTGAGTTG GAACCAAGAA GAAATTCAAG AAATTGGAA  
 3351 GAAATCATCC CAGAACATCCA ACAGGAGAAGG ATAGAGGAGG AGGAAAGACA  
 3401 AAAAGAACTT GAAGAAATAT ACATGCTCCC GAGGATGAGA AACTGTCAA  
 3451 AACAGATCAG CTTAATGGG AGTGAAGGAA GACGAGTAG GAGCAGAAGA  
 3501 TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAC GGCCAAAAAA  
 3551 GCGTGGAAAGA CCTCGAACCA TTCCCTCGAGA AAAATATTTAA GGATTTAGT  
 3601 ATGCAGAGAT CAGGCCGTTT ATCAAGAGTT ACAAGAAATT TGGTGGCCCT  
 3651 CTGGAAAGGT TAGATGCTGT AGCTAGAGAT GCTGAACCTGG TTGATAAATC  
 3701 TGAGACAGAC CTTAGACGTT TGGGTGAAC TGACATAAT GGATGCATTA  
 3751 AGGCTTTAAA GGACAATTCA TCTGGACAAG AAAGAGCAGG AGGTAGACTT  
 3801 GGGAAAGTT AAGGCCAAC GTTTCGAATC TCAGGAGTGC AGGTGAATGC  
 3851 AAAACTAGTC ATCTCTCACG AAGAAGAGCT GGCAACACTG CACAAATCCA  
 3901 TTCCCTCAGA TCCAGAAAGAA AGGAAAAGAT ATGTCATCCC ATGCCACACC  
 3951 AAGGCTGCTC ACTTCGATAT AGATTGGGT AAAGAAGATG ATTCCAAATCT  
 4001 GTTAGTAGGC ATCTATGAAT ATGGCTATGG CAGCTGGGAA ATGATAAAA  
 4051 TGGATCCAGA TCTCAGCTTA ACACAGAAAGA TTTTACCTGA TGATCCAGAC  
 4101 AAGAAACCCC AGGCAAAGCA GCTACAGACC CGTGCAGACT ACCTCATTAA  
 4151 ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAAGG CTTGCTGGTG  
 4201 CAGGCAATTCA CAAGAGAAGG AAGACAAGAA ATAAGAAGAA TAAGATGAA  
 4251 GCTTCAAAAA TAAAAGAAGA AATAAAAGAGT GATTCTTCAC CACAACCC  
 4301 AGAAAATCT GATGAAGATG ATGAGGAGGA GGATAACAAG GTAAATGAA  
 \*\*\*  
 4351 TGAAATCTGA AAATAAAAGAA AAATCTAAA AAATTCCATT GCTGGATACT  
 4401 CCAGTCATA TTACTGCAAC CAGTGAACCA GTTCCTATCT CAGAAGAAC  
 4451 TGAAGAACTC CATCAGAAGA CATTAGTGT GTGCAAAGAA AGAATGAGGC  
 4501 CTGTCAAAGC ACCACTGAAA CAGCTGGATA GACCAGAGAA GGGCCTTCT  
 4551 GAAAGGGAGC AGCTGGAACA TACTAGGCAG TGTCTAATCA AAATTGGGA  
 4601 TCACATTACA GAATGCCTGA AGGAGTACAC AAATCCGAG CAAATAAAC  
 4651 AGTGGAGGAA AAATTGTGG ATTTTGTGT CCAAGTTTAC AGAATTGAT  
 4701 GCCAGAAAGC TCCACAAACT CTACAAACAT GCAATCAAAA AGCGCCAAGA  
 4751 GTCTCAGAAC CACAATGACC AAAACATTAG CACCAATGTG AATACACATG  
 4801 TAATCAGAAA TCCAGATGTG GAAAGACTGA AGGAGACTAC AAACCATGAT  
 4851 GATAGTAGCA GGGACAGTTA TTCTTCTGT AGACATTTAT CACAATACCA  
 4901 TGATCATCAC AAAAGACAGGC ATCAGGGAGA TGCTTACAAG AAAAGTGA  
 4951 CCAGGAAAGG GCCATATTCA GCCTTCAGTA ATGGAAAAGA TCACAGAGAC  
 5001 TGGGATCACT ACAAAACAGGA CAGCAGATAC TACAGTGATA GTAAACATAG  
 5051 AAAGTTAGAT GACCACAGGA GCAGAGACCA CAGGTCAAAC CTGGAAGGAA  
 5101 ACTTAAAAGA CAGCCGGGGT CATTCAAGTC ACCGCTCCC TTCAGACC  
 5151 AGGATACACT CAGATCACCG TTCCACTTCA GAATACAGCC ATCATAAATC  
 5201 TTCGAGAGAT TATAGATACC ACTCAGACTG GCAAATGGAC CACAGAGCTT  
 5251 CTGGTAGTGG CCCGAGGTCA CCACTAGATC AGAGGTCTCC TTATGGTCA  
 5301 AGATCTCCCC TAGGACACAG ATCTCCATT GAAACACTCAT CAGATCACAA  
 5351 AAGTACACCT GACACATACAT GGAGTAGCCG GAAGACATAA CAAAGACTGA  
 5401 CATTTCCTGG ACCTTCTTT TAGCCATATA CAGTAAACTA ACACAGTAAT  
 5451 TGCCTTACAT GACTTGAAAG ATATGGACTG GATATTCTAT CAGTAGCA  
 5501 ATTGTTACTT CTTTCCAGGA TGCAAGGTCT ATTATCCAA CAGAAGAAAA  
 5551 ATATTTTGT ATTTAAAGTT TATGCTGCAC TGTGCTGAA ATGTTGTGGC  
 5601 ACTTTTTTT TAAGAAATGG AAGATGTTA CTTTACAGG GACCTCAACA  
 5651 CTGCCCTTT CAGACTGGAT CTTACTATAA AACTCTTCAT GTCAAAGTGG  
 5701 TTCTAGGTG AACACAGATT AAATTATGTT TGAAATGAA CACTTAAACA  
 5751 CTGACCTGTG CTATGTTC AGGAAAGAAT GGGGATTAA TTTTGTTTA  
 5801 TTTCTGGTA GAGAACCTCTC AAGGACTTTG TTCACTTTCC AAAGCTACTT  
 5851 GTTTACATTG TACACTGCGA CCACCTTGC GCTTTCATC ACAAGCTTGA  
 5901 ATATTAAAT TCTGTACCTA CAGTTGAAA ATAGCCAGGA TTTCTCTGT  
 5951 TTGTGATCAG TTATAATGCC TTTTTATGAA ACAAAACAAAC AAACAAAAAA  
 6001 CAATTAAAAA AAAAAACACA ACAAAACAA CAAATGGCTG TAAATTATTG  
 6051 TAAATAATT AAATGAGCTT TTTCCGTCA GGCTTTTTT GGCTGTTCT  
 6101 TTCCCCAACAA ACTCAGGCC TCTTTTCAAA AAGTCAGTAT ACTTACATGT  
 6151 TTTAATAAAAA TATCTCGATG GAATCAGAAT GTAAAAATGG GGAAGGGAA  
 6201 ATTTTATTCC ATTTAGTGCT CCTTTTTTAT TGGATACTTT TACATACCTG  
 6251 TTTTGGTTG TTTTATTATA TTTTTTTTT CTATTAACACT GTCAGTGTG  
 6301 TGATTGTTG AATGAACAGT GAGAATATCC CACTCTAAAC TGTGCCCTGG  
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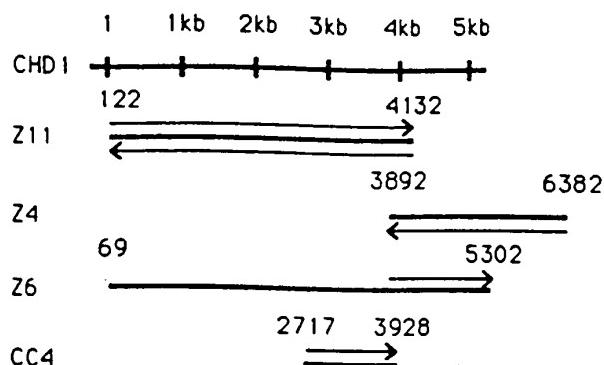
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6401 ACACATTCAAA ACCCAGATCA GCCAAGATTG ATTGTAAATC CATTGGTTTT  
6451 CCCTCTTAA CATGGGCAAT AATGTCAAAT GTGCTATGCA GCAGTTAATA  
6501 TTTTAGAAGA TTGGAATGAC TTTATTAACA GAATTGTTAC AATGCACACT  
6551 GATTGTACAT AGATAACTTC TATCTGACAA ATAAATTAA CTAAAACCAA  
6601 AAAAAACC

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**Figure 6.**



**Figure 7.**

	D E I V S V K H L H K K I K T E
<i>CBD-1A</i>	1 GATGAGATTGTTTCAGTGAACATCTACATAAAAAAAATAAAAACAGAAA
<i>CBD-W</i>	1 GATGGGATTGTTTCAGTGAACATCCACATAAAAAAAATAAAAGCAGAAA D G I V S V K H P H K K I K A E
	K E N E E K P E P D I G I K K E A
<i>CBD-1A</i>	51 AAAGAAAATGAAGAAAAGCTGAGCCAGATTTGGTATAAAGAAGGAAGCT
<i>CBD-W</i>	51 AAAGAAAATGAAGAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCT K E N E E K D E P E I G I K K E A
	E E K R E T K E K E N K R E L K R
<i>CBD-1A</i>	101 GAAGAAAAAAGAGAGACAAAAGAGAAGGAAAATAAGGGATTGAAAAGG
<i>CBD-W</i>	101 GGAGAAAAAAGAGAGACAAAAGAAAAGGAAAATAAGA G E K R E T K E K E N K
	E K K E E K E D K K E L K E K D N K
<i>CBD-1A</i>	151 GAGAAAAAAGAAAAAGAGGATAAGAAAAGAATTAAAAGAAAAAGATAATAAA
	E K R E N K V K E S T Q R E K E V
<i>CBD-1A</i>	201 GAAAAGAGAGAAAACAAGTAAAAGAATCCACACAGAAAGAAAAAGAAGTG
	K E E K
<i>CBD-1A</i>	251 AAGGAAGAGAGAAG

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Figure 8.

ATPTATCGGC TAGTCACAAA AGGATCAGTA GAAGAAGATA TTCTTGAAAG AGCCAAGAAA AAGATGGTGT TAGATCATTT  
10 20 30 40 50 60 70 80  
AGTGATTCAAG AGAACATGGACA CCACACGGAA AACATGACTA CATAACAGGCT CTACTCCCTC AAGCTAACCA CCTTTTAATA  
90 100 110 120 130 140 150 160  
AGGAAGAGTT ATCAGCAATT TTGAAGTTG GTGCTGAGGA ACTTTTTAAA GAACCTGAAN NNGAAGAAGA GGAGCCCTCAG  
170 180 190 200 210 220 230 240  
GAGATGGATA TAGATGAAAT CCTGAAGAGG NCTGAAACTC GAGAAAATGA GTCAGGCCCA TTAACGTAG GAGATGAGTT  
250 260 270 280 290 300 310 320  
ACTTTCACAG TTCAAGGTAG CTAACCTTTC CAATATGGAT GAAGATGACA TTGAATTGCA ACCAGAACAA AATCTAAGAA  
330 340 350 360 370 380 390 400  
ACTGGGAAGA AATCATTCGA GAAGTTCAAGT GGCGACGAAT AGAGGGGNNG GAAAGACAAA AAGAACCTGA AGAAATATAT  
410 420 430 440 450 460 470 480  
ATGCTTCCAA GAATGAGAAA CTGTGCAAAA CAGATCAGCT TTAATGGAAA TGAAAGGAGA TGCAGTAGGA CCAGAACAGA  
490 500 510 520 530 540 550 560  
TTCTGGATCT GATAGTGTGATT CCATCTCAGA AAGAAAAACGA CCAAAAAAAC GTGGACGACC ACCAACTATT CCCCGTGAAA  
570 580 590 600 610 620 630 640  
ACATTAAGG ATTTAGTGTG GCAGAGATTA GACGATTAT CAAGAGTTAC AAGAAATTG TGCCCCAGT TGAAAGGTTA  
650 660 670 680 690 700 710 720  
GATGCTATAG CTAGAGATGC TGAGCTAGT GATAAAATCTG AAACAGACCT TAGACGTCG GGAGAACTTG TACATAATGG  
730 740 750 760 770 780 790 800  
ATGCATTAAG GCTTTAAATG ATAATGACTT TGGTCAAGGA AGAACAGGTG GTAGATTG GAAAGTTAAA GGCCCAACAT  
810 820 830 840 850 860 870 880  
TCCGAAATACC AGGAGTCAG GTGAATGCAA AGCTAGTCAT TTCTCACGAA GAAGACTTOG CACCATGCA TAAATCGATT  
890 900 910 920 930 940 950 960  
CCTTCAGATC CAGAAGAAAG GAAAAGATAT GTCATCCCAT ACCACACCAA AGCAGCTCAT TTGATATAG ATTGGGGTAA  
970 980 990 1000 1010 1020 1030 1040  
AGAAGATGAT TCCAATCTGT TAATAGGCAT CTATGAATAT GGTTATGGCA GTGGGAAAT GATAAAATG GATCCTGATC  
1050 1060 1070 1080 1090 1100 1110 1120  
TCAGTTGAC ACAGAAAGATT TTACCTGATG ATCCAGATAA GAAACCCCAAG GCTAACGAGT TACAGACTOG TCCAGATTAC  
1130 1140 1150 1160 1170 1180 1190 1200  
CTCATTAAT TACTGAATAA AGACCTTGCA AGAAAGGAAG CACAGAGACT TGCTGGTGCA GGCAATTCAA AGAGGAGAAA  
1210 1220 1230 1240 1250 1260 1270 1280  
AACAGAAAGT AACAGAAATA AACCAACAAA CGCTGC  
1290 1300 1310

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Figure 9.

<i>C CHD-1A</i>	DARRYLGKNLGHL*RIASQTHYFENIRSTRKGILDHLVT*VDFLFNFILITMNGSDEE
<i>M CHD-1</i>	FALCPPVTQREPQETRECRKIFIEILIFEKICIEHLLIGDFCFINFLIFTMNGSDEE
<b>*****</b>	
<i>C CHD-1A</i>	SVRNSSGESSRSDDDSAGSGSGSGSSSGSSSDGSSSQGSSDSESGSESGSQSESES
<i>M CHD-1</i>	SVRNGSESSQSGDD-CGSAGSGSGSSSGSSSDGSSSQGSSDSDSGSQSESES
<b>*****</b>	
<i>C CHD-1A</i>	TSREKKVQAKPPKADGSEFWKSSPSILAVQRSAVLKKQQQQ--QKAASSDSCGSEEDSS
<i>M CHD-1</i>	TSRENK-VQAKPPKVDGAEFWKSSPSILAVQRSAMLRKQPOQAQQQRPASSNSGSEEDSS
<b>*****</b>	
<i>C CHD-1A</i>	SSEDSADDSSSETKKKKHDKEDDWOMSGSGSVGTGDSSESAEDGDKSSCEEESDYEPKN
<i>M CHD-1</i>	SSEDS-DDSSSGAKRKKHDKEDDWOMSGSGSPSQLGSDSEEEERDKSSCDGTESDYEPKN
<b>*****</b>	
<i>C CHD-1A</i>	KVKSRSKPPSRIPKPGKKSTGQKKRQLDSSEEEEDDDEDYDKRGSRQATVNVSYKEAZZ
<i>M CHD-1</i>	KVRSRKPNRNSKSNKGKKILGQKKRQIDSSEEEEDDEDYDKRSRQATVNVSYKEDEE
<b>*****</b>	
<i>C CHD-1A</i>	TKTDSDDLLEVCGEDVPQTEDEFETIEFKMDRSRIGRKGATGASTTIYAVEADGDPNAGF
<i>M CHD-1</i>	MKTDSDDLLEVCGEDVPQPEDEFETIERVMDCRVRKGATGATTIYAVEADGDPNAGF
<b>*****</b>	
<i>C CHD-1A</i>	KTXERGEIQLIKWKGWSHIHNWETEETLQQNV/RGMOKLDNYKKDQEETKRWLKNAS
<i>M CHD-1</i>	EKSKELEGEIQLIKWKGWSHIHNWETEETLQQNV/RGMOKLDNYKKDQEETKRWLKNAS
<b>*****</b>	
<i>C CHD-1A</i>	ERNEKEGDIOIQLIKWKGWSHIHNWETEETLQQNV/RGMOKLDNYKKDQEETKRWLKNAS
<i>M CHD-1</i>	<b>[REDACTED]</b>
<b>*****</b>	
<i>HUMAN</i>	PEDVEYYNCQQELTDDLEHKQYQIVERTNXSFQSKSAAGP
<i>C CHD-1A</i>	PEDVEYYNCQQELTDDLEHKQYQIVERILAESNQSKSAAGYPDYCKWQGLPYSECWSWEGA
<i>M CHD-1</i>	PEDVEYYNCQQELTDDLEHKQYQIVERILAESNQSKSAAGLPDYCKWQGLPYSECWSWEGA
<b>*****</b>	
<i>C CHD-1A</i>	LIAKKFQARIDEYSRNQSKTTPFKDCVKLQRPRFVALKKQPSYIGGHE <del>SLELRDYQLN</del>
<i>M CHD-1</i>	LISKKFQTCIDEYSRNQSKTTPFKDCVKLQRPRFVALKKQPSYIGGHE <del>GELRDYQLN</del>
<b>*****</b>	
<i>C CHD-1A</i>	GLNWLAHSWCKGNSCI LADEMGLGKTIQTISFLNLYLHFEBQLYGPFLRVPLSTLT
<i>M CHD-1</i>	GLNWLAHSWCKGNSCI LADEMGLGKTIQTISFLNLYLHFEBQLYGPFLVVPLSTLT
<b>*****</b>	
<i>C CHD-1A</i>	EIQTWAQMNAAVYLGIDITSRNMIRTHEWMHPQTKLKPNIILLTTYEILLKD
<i>M CHD-1</i>	EIQTWAQMNAAVYLGIDINSRNMIRTHEWMHPQTKLKPNIILLTTYEILLKD
<b>*****</b>	
<i>C CHD-1A</i>	WAFIGVDEAHLRNDDSSLYYRTLIDFKSNHRLLTGTPLQNSLKEWLSSLEFIMPEKFSS
<i>M CHD-1</i>	WAFIGVDEAHLRNDDSSLYYRTLIDFKSNHRLLTGTPLQNSLKEWLSSLEFIMPEKFSS
<b>*****</b>	
<i>C CHD-1A</i>	WEDFEEEBGKGREGYASLHKLEPFLLRRVKKDVKSILPAKVEQILRMEMSAQKQYYK
<i>M CHD-1</i>	WEDFEEEBGKGREGYASLHKLEPFLLRRVKKDVKSILPAKVEQILRMEMSAQKQYYK
<b>*****</b>	
<i>C CHD-1A</i>	WILTRNYKALSKGSKGSTSGLNIMMELKKCCNCYLIKPDDNEFYNKQEAQHLIRSS
<i>M CHD-1</i>	WILTRNYKALSKGSKGSTSGLNIMMELKKCCNCYLIKPDDNEFYNKQEAQHLIRSS
<b>*****</b>	
<i>C CHD-1A</i>	GKLILLDKLIRRERGNRVLIFSQMVRMLDILAELYKRYQPPPQRLDGSIKGELRKQAL
<i>M CHD-1</i>	GKLILLDKLIRRERGNRVLIFSQMVRMLDILAELYKRYQPPPQRLDGSIKGELRKQAL
<b>*****</b>	

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C CHD-1A  
M CHD-1DEFNAECSDFCFILLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQV  
DEFNAECSDFCFILLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQV  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1-IYRLVTGKGSVEEDILERAKKMVLDELVQMDTTGKTVLTGSTOPSSSTPNKEELSA  
NIYRLVTGKGSVEEDILERAKKMVLDELVQMDTTGKTVLTGSTOPSSSTPNKEELSA  
NIYRLVTGKGSVEEDILERAKKMVLDELVQMDTTGKTVLTGSTOPSSSTPNKEELSA  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1ILKFGAEELFREPXEKEEEEPQEMDIIDEILKRXETRENESGPLTVGDELLSQFKVANPSNM  
ILKFGAEELFREPXEKEEEEPQEMDIIDEILKRAETHEENEPGPLSVGDELLSQFKVANPSNM  
ILKFGAEELFREPXEKEEEEPQEMDIIDEILKRAETRENEPGPLTVGDELLSQFKVANPSNM  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1DEDDIELEPEQNLRNWEIIPEVQWRRIEGXERQELEEYIMLPRMRNCAQISFNGREG  
DEDDIELEPERNSRNWEIIPEEQRRLKEERQELEEYIMLPRMRNCAQISFNGSEG  
DEDDIELEPERNSRNWEIIIPESORRRIEERQELEEYIMLPRMRNCAQISFNGSEG  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1RCRSRYSGSDSDSISERKRPKGRPRTIPRENIKGFSDAEIRRPIKSYKPGGPVER  
RRSRYSRYSGSDSDSISERKRPKGRPRTIPRENIKGFSDAEIRRPIKSYKPGGPVER  
RRSRYSRYSGSDSDSISERKRPKGRPRTIPRENIKGFSDAEIRRPIKSYKPGGPVER  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1LDALARDAAELVDKSETDLRLRGELVHNGCKALNDNDFOQGRGGTGRPGKVGPTRIAGV  
LDALARDAAELVDKSETDLRLRGELVHNGCKALKDSSGTERAGGRGLGVGPTRISGV  
LDAVARDAELVDKSETDLRLRGELVHNGCKALKDNNSSQERAGGRGLGVGPTRISGV  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1QVNAKLVISHEEEELAPLHKSI PSDPEERKRYVIPHETKAHFIDWKGEDDSNLLIGIYE  
QVNAKLVIAHEDELIPLHKSI PSDPEERKQYTI PCBTKAHFIDWKGEDDSNLLIGIYE  
QVNAKLVISHEEEELAPLHKSI PSDPEERKRYVIPHETKAHFIDWKGEDDSNLLVGTYE  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1YGYGSWEIMKMDPDLSTQKILPDDDKPKAQQLQTADYLILLLNKDLARKEAQRLAG  
YGYGSWEIMKMDPDLSTHKILPDDDKPKAQQLQTADYLILLLNKDLARKEAQRLAG  
YGYGSWEIMKMDPDLSTQKILPDDDKPKAQQLQTADYLILLLNKDLARKEAQRLAG  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1AGNSKRRKTRSKKNNKATKA  
AGGSKRRKTRAKKSKAMKSIVKKEEIKSDSSPLPSEKSDDEDD---KLNDSPKESKDRS  
AGNSKRRKTRNNKNNK-MKASKIKEEIKSDSSPQPKSEKSDDEDEEDNKVNEMKSENKEKS  
\*\*\*\*\*C CHD-1A  
M CHD-1KKSVVSDAPVHITASGEPPVPIAESEELEDQKTFSICKERMRPVKAALKQQLDPEKGLSER  
KKIPLLDTPVHITATSEPPVPISEEESEELEQKTFSVCKERMRPVKAALKQQLDPEKGLSER  
\*\*\*\*\*C CHD-1A  
M CHD-1EQLEHTROCLIKIGDBITECLKEYSNPEQIKOWRKNLWIFVSKTFDARKLHLKLYKAI  
EQLEHTROCLIKIGDBITECLKEYTNPEQIKOWRKNLWIFVSKTFDARKLHLKLYKAI  
\*\*\*\*\*C CHD-1A  
M CHD-1KKRQESQNSDQN-SNVATTIVIRNPDMERLKENTNHDDSSRDSYSSDRHLSQYHDHHD  
KKRQESQENDQNINNSNVNTVIRNPDMERLKENTNHDDSSRDSYSSDRHLSQYHDHHD  
\*\*\*\*\*C CHD-1A  
M CHD-1RHQGDSYIKSDSRKRYPYSSPSNGKDEREWHDYRQDGYYSDREKERKLDDERSRERPSL  
RHQDAYKSDSRKRYPYSAFSNGKDERWDHYKQDSRYYSDS-KERKLDDERSRERPSL  
\*\*\*\*\*C CHD-1A  
M CHD-1EGGLKD-RCHSDHRSBSDLRHMHSDEHRSRSTPSTHINPPRDYRYLSDWQLDERAASSGPRSP  
EGNLKDSDRGHSDHRSBSDLRHMHSDEHRSRSTSEYSHKSSRDYRYHSDWQMDERASGSGPRSP  
\*\*\*\*\*C CHD-1A  
M CHD-1LDQRSPYGSRSP-----FEHSAEHRSTPETHWSRKTXQKLMSSLSSGTLXP  
LDQRSPYGSRSPLGHRSPFEHSSDHKSTPETHWSRKTXQRLTSGPSXPYTVNXBSNC  
\*\*\*\*\*C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1ALTXLERYGLDILSVAVLILSRSRMOGLLSQKRNIFVVKVYAAALCCRCGTFPLRNRCLL  
LOGPO8CPFTGTSYKTLHVVKVULGXTOIKLCXLXMTXTLTCAVSGJGNGGPILFYFLVE  
NSQGLCSLSKATCLBCRTLPPCRFSQAXIPKFCCTYSCKLARIJPVCDCQDXCLPMQTK  
QKTIKKMTTKPTNCKLXXINMXMSFFPSGFPLWFLSPTTQAFPSQSQYTYMIXNISME  
SECKNGEYNILPHVLPYWLLETCTWLFLPYFIPFYXTVSVVVMNSENIPLXTVWPW  
AFQVHWPKRRKCSIGEHTQISQDSXILHPSLNMGNVVKAMQOLIPXKIMTLLTE  
LLOQTLIVRXLSDKLNLXLCPKKT

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Figure 10.

55 KPPKADGSEFWKSSPSILAVQRSAVLKKQQQQKAASSDSCSEEDSSSE 104  
 2654 MAAKDISTEVLQN.PELYGLRRS...HRAAAHQNYFNDSDDEDD....E 2695

105 DSADDSSSETKKKKHKDEDWQMSGGSVSGTGSDSESAEDGDKSSCEESE 154  
 2696 DNIKQSRRKRMTTIEDDED.....EFEDEEGEEDSGEDEDEDFEEDD 2738

155 SDYEPKNVKSRKPPSRIPKSGKSTGOKRQLDSSEEEEDDEDYDKR 204  
 2739 DYVGSPIKQNRSKPKSRKSKSKPKSQEKQSTVKIP.....TRF 2780

205 GSRRQATVNVSYKEAEETKTDSDDLLE...VCGEDVPQT....EEDEFE 246  
 2781 SNRQNKTVDNYNIDYSDDDLLESEDDYGSEEALSEENVHEASANPQPEDFH 2830

247 TIEKFMDSRIGRKATGASTTIYAVEADGDPAGFEKSKELGELIQYLIKW 296  
 2831 GIDIVINHRL.....KTSLEEGKVLEKTVPDLNNCRE..NYEFLIKW 2870

297 KGWSHIBNTWETEETLKQONVKGMNKLDNYKKK...DQEETKRWLKNASPE 343  
 2871 TDESHLBNTWETYESIGQ..VRGLKRLDNYCKQFIIEDQQVRLDPYVTAE 2918

344 DVEYYNCQQELTDDLHKQYQIVERIIA..HSNQKSAAGYPDYCKWQGLP 391  
 2919 DIEIMDMERERRLDEFEEFHVPERIIDSQRASLEDGTSQLQYLVKWRRLN 2968

392 YSECWSWEDGALIAKKFQARIDEYFSRNQSCKTPFKDCVKLQRPRFVALK 441  
 2969 YDEATWENATDIVKLAPEQVKHFQNRENNSKILPQYSSNYTSQRPRFEKLS 3018

442 KQPSYIGGHESLELRDYQLNGLNWLAEHWCKGNSCILADEMGLGRTIQTI 491  
 3019 VQPPFIKG...ELRDFQLTGINWMAFLWSKGDNGLILADEMGLGKTVQTV 3065

492 SFLNYLFHEHQLYGPFLLRVPLSTLTSWQREIQTWAPQMNAVYLGDIS 541  
 3066 AFISWLIFARRQNGPHIIVVPLSTMPAWLDTFEKWADLNCICYMGNQKS 3115

542 RNMIRTHEW....MHPQTKRLKFNILLTYEILLKDKSPLGGLNWAFIGV 587  
 3116 RDTIREYEFTNPRAKGKTMKPVNLLTTYEYLKDRAELGSIKWQFMAV 3165

588 DEAHLKLNDDSLLYRTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPE 637  
 3166 DEAHLKLNAESSLYESLNSPKVANRMLITGTPLQNNIKELAALVNPLMPG 3215

638 KFSSWEDFE.EEHGKGREYGYASLHKELEPFLLRRVKKDVEKSLPAKVEQ 686  
 3216 RFTIDQEIDFENQDEEQEEYIHDLRRIQPFILRRLKKDVERSLPSKTER 3265

687 ILRMEMSALQKQYYKWLTRNYKALSKGSKGSTSGFLNIMMELKKCCNHC 736  
 3266 ILRVELSDVQTEYYKNILTKNYSALTAGKGGHFSLLNIMNELKKASNHP 3315

737 YLIKPPDDNEF.....YNKQEALQBLIRSSGKLILLDKLLIRLRERGN 779  
 3316 YLFDAEERVLQKFGDGKMTRENVLRGLIMSSGKVMLLDQLLTRLKKDGB 3365

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780 RVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHFNAEGS 829  
 3366 RVLIFSQMVRMLDILGDYLSIKGINFQRLDGTVPSAQRRISIDEFNSPDS 3415  
 830 EDFCFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKK 879  
 3416 NDFVFLLSTRAGGLGINLMTADTVVIFDSDWNPQADLQAMARAHRIGQKN 3465  
 880 QVNIVYRLVTKGSVEEDILERAKKRMVLHDLVIQRMDDTTGKTVLHTGSTPS 929  
 3466 EVMVYRLVSKDTVEEEVLERARKMILEYAIISLGVTDGNKYTKKNEP.. 3513  
 930 SSTPFNKEELSAILKFGAEELFKEPEGEQEPEQEMDIDEILKRAETRENE 979  
 3514 ....NAGELSAILKFGAGNMFTATD.NQKKLEDLNLDLVNLNAEDHVTT 3557  
 980 PG...PLTVGDELLSQFKVANFSNMDEDIELEPERNSRNWEIIPESQR 1026  
 3558 PDLGESHLGEEFLKQFEVTDY.....KADIDWDDIIPPEEEL 3594  
 1027 RRIEEEERQKELEE....IYMLPRMRNCAKQI..SFNGSE..... 1060  
 3595 KKLQDEEQKRKDEEYVKEQLEMMNRRDNALKKIRKNSVNGDTAANSDD 3644  
 1061 ..GRRSRSRYYSGSDSDSITERKRPKRRGRPRTIPR.ENIKGFS...AE 1104  
 3645 DSTSRSSRRRARANDMDSIGE...SEVRALYKAILKFGNLKEILDELIAD 3691  
 1105 IRRFIKSYKKFGGLERLDAVARDA.....ELVDKSETDLRRLGEL 1145  
 3692 GTLPVKSFEKYGETYDEMMEAAKDCVHEEEKNRKEILEKLEKHATAYRAK 3741  
 1146 VHENGCIAKLD.NSSGQERAGGRGLGVKGPTFRISGVQ.VNAKLVISHEE 1193  
 3742 LKSGEIAENQPKDNPLTRLSLKKREKKAVALFNFKGVKSLNAESLLSRVE 3791  
 1194 ELAPLHKSI PSD.PEERKRYVIPCHTKAA..HFIDIWGKEDDSNLLVGIY 1240  
 3792 DLKYLKLNLSNYKDDPLKFLGNNTPKPVQNWSNNWTKEDEKLLIGVF 3841  
 1241 EYGYGSWEMIKMDPDLSLTQKILPDD..... 1266  
 3842 KYGYGSWTQIRDPPFLGITDKIFLNEVHPVAKKSASSSDTTPTPSKKGK 3891  
 1267 .....PDKKPQAKQLQTRADYLIKLLNKDLARK.....EAQRLAGAGNS 1305  
 3892 GITGSSKKVPGIAHLGRRVDYLLSFLRGGLNTKSPSADIGSKKLPTGPSK 3941  
 1306 KRRKTRNKKNMKASKIKEEIKSDSSPOPSEKSDEDDEE..EDNKVNEM 1352  
 3942 KRQRKPNHSKSMTPEITSSEPANGPPSKRMKALPKGPAALINNTRLSPN 3991  
 1353 KSENKEKSKKIPLLDPVHITATSEPVPISEESEELHQKTFSVCKERMRP 1402  
 3992 SPTPPLSKVSRDNGTR....QSSNPSSGSAHEKEYDSMDEEDCRBTMSA 4037  
 1403 VKAALKQLDRPEKGLSEREQLBETRQCLIKIGD8ITECLKEYTNPEQIKQ 1452  
 4038 IRTSLKRLRRGGKSLDRKEWAKILKTELTTIGNBI.ESQKGSSRKASPEK 4086  
 1453 WRKNLWIFVSKP..TEFDARKLHKLYKHAIIKKRQESQQ 1488  
 4087 YRKHLWSYSANFWPADVKSTKLMAMY....DKITESQK 4120

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Figure 11.

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CCHD	AVEAD	GDPNAGFEKSKELG . IQYLIKWKGSIHNTWE TEET	LKQQNVGMNKLDNYKK
MCHD	AVEAD	GDPNAGFERNKEPGD . IQYLIKWKGSIHNTWE TEET	LKQQNVGRGNKKLDNYKK
YCHD	EGKVL	EKTVPDLNNCKE .. N . YEFLIKWTDESHLHNTWETYES	IGO . VRGLKRLDNYCK
		** * * * * * * * * * * * * * * *	* * * * * * * * *
DHP1	EEEEEE	YAVEKIIIDRRVRKGK . VEYLLWKGYPETENTWEPEENN	LDCQDLIQQY
BHP1	EDEEE	YYVEKVLDERRVVKGK.QVEYLLWKGFSEEHNTWEPEKN	LDCPELISEF
MMOD1	EEEEEE	YYVEKVLDERRVVKGK . VEYLLWKGFSDEDNTWEPEEN	LDCPDLIAEF
MMOD2	AEPEE	FVVEKVLDERRVVNGK . VEYFLWKGFDTDADNTWEPEEN	LDCPELIEDF
		** * * * * * * * * * * * * * * *	* * * * *
DPC	PVDLV	YAAEKIIIQKRVKKGV . VEYRVWKWNQRYNTWEPEENN	ILDRLRIDLIV
MMOD3	VGEQV	FAAACILSKRLRKKGK . LEYLVKWRGWSKENSWEPEEN	ILDPRLLLAF
		* * * * * * * * * * * * * * * *	* * * * *
			^ ^

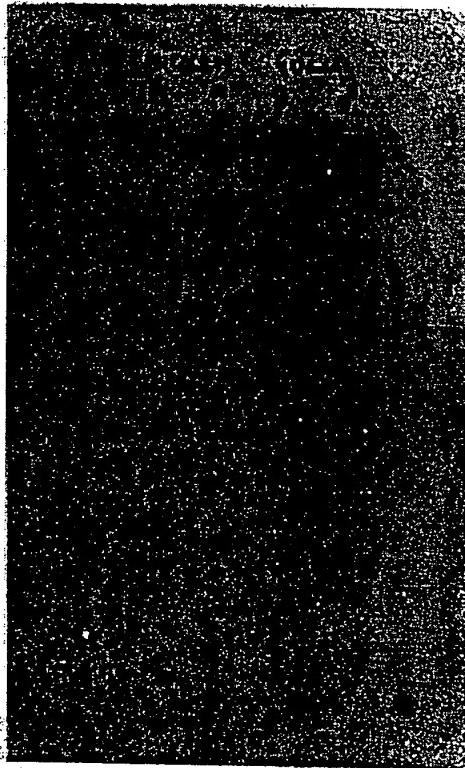
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Figure 12.



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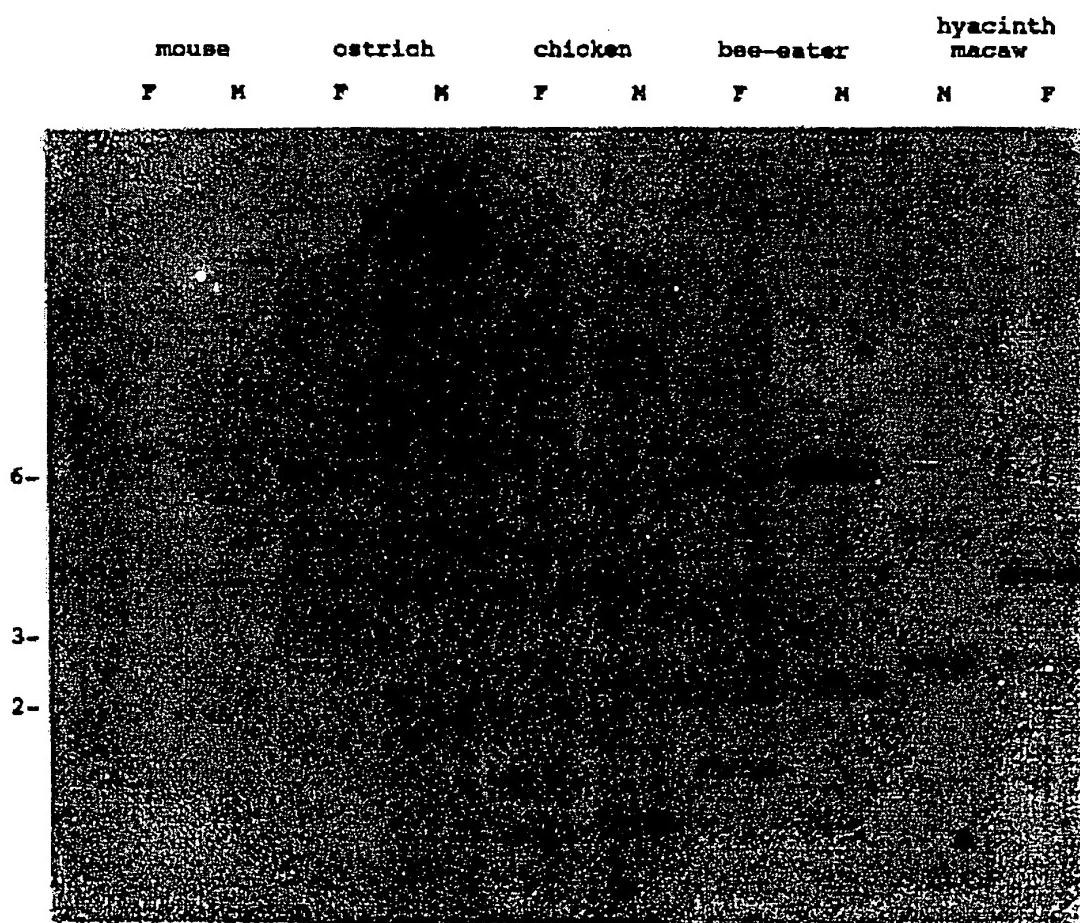
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Figure 13.



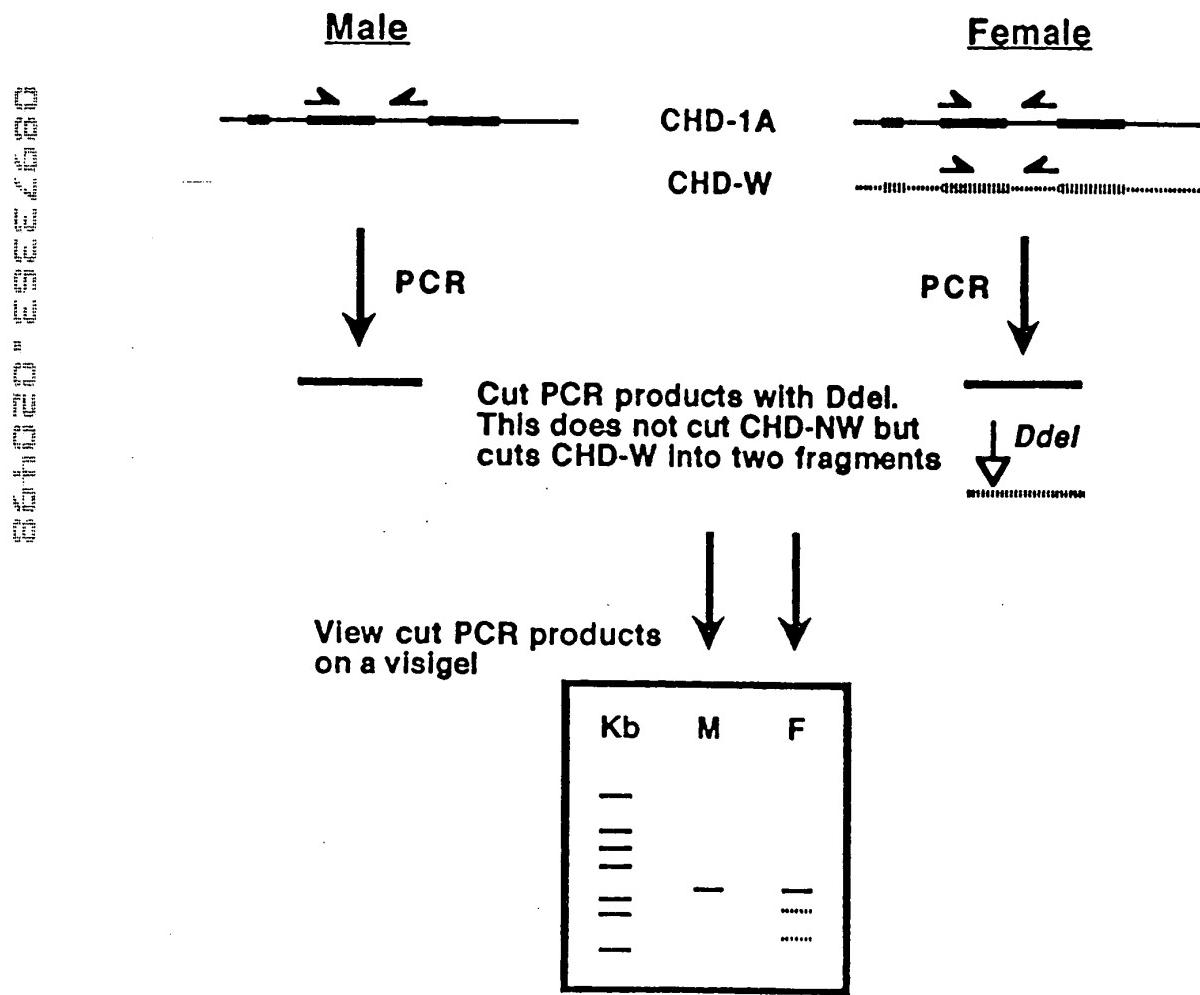
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Figure 14.

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MOUSE	CHD1	AGA TAT TCT GGA TCT GAT AGT GAT TCA ATC TCG GAA
CHICKEN	CHD-1A	--- --- --- --- --- --- C --C --- A-A ---
SPIX	CHD-1A	C --C ---
CHICKEN	CHD-W	--- --- --- --- --- --- --C --- --A ---
SPIX	CHD-W	C --C --- --A ---
HYACINTH	CHD-W	C --C --- --A ---
P1		C --C --- --A ---
P3		A TAT TCT GGA TCT GAT AGT GAT GAY TC
		AGA TAT TCC GGA TCT GAT AGT GA
MOUSE	CHD1	AGG AAA CGG CCG AAG AAA CGT GGG CGA CCC CGC ACT
CHICKEN	CHD-1A	--A --- ---A --A --G --- --A A-- --T --A --C
SPIX	CHD-1A	--- --- ---A --A --G --- --A A-- --A --A ---
CHICKEN	CHD-W	--A --- --A --A --A --- ---A --- --A --A ---
SPIX	CHD-W	--A --- --A --A --GA --- ---A --- --A --A ---
HYACINTH	CHD-W	--A --- --A --A --- ---A --- --A --A ---
MOUSE	CHD1	ATC CCT CGG GAG AAT ATT AAA GGA TTT AGT GAT GCG GAG
CHICKEN	CHD-1A	--T --- --A --A --- --- --- --- --- ---A ---
SPIX	CHD-1A	--T --- --A --A --- --A
CHICKEN	CHD-W	--T --C --T --A --C --- --- --- --- ---A ---
SPIX	CHD-W	--T --- --T --A --- ---
P2		TTT CCT AAA TCG CTA CGT CT
HYACINTH	CHD-W	ATT AGG CGG T
HYACINTH	CHD-W	--- --- --- --- ---C --- --A --G

Figure 15.



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Figure 16.

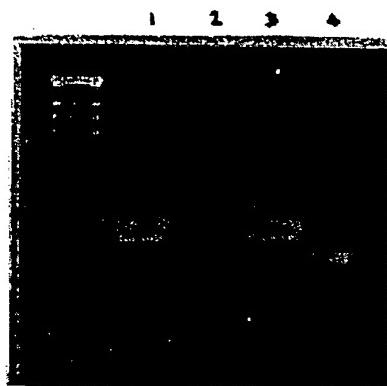
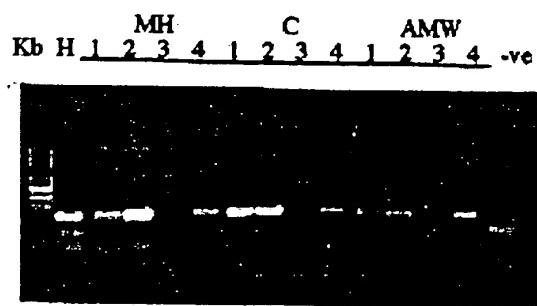


Figure 17.



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